

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/201,916

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/201,916DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>

Does Not Comply
Corrected Diskette Needed

PR 3-4

```

1  <110> APPLICANT: Hope, Ralph Graham
2      McLauchlan, John
3  <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
4  <130> FILE REFERENCE: DYOU17.001AUS
5  <140> CURRENT APPLICATION NUMBER: US/09/201,916
6  <141> CURRENT FILING DATE: 1998-12-01
7  <160> NUMBER OF SEQ ID NOS: 13
8  <170> SOFTWARE: FastSEQ for Windows Version 3.0
9  <210> SEQ ID NO 1
10 <211> LENGTH: 630
11 <212> TYPE: DNA
12 <213> ORGANISM: Hepatitis C Virus
13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (43)...(630)
16 <400> SEQUENCE: 1
17      ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat      54
18                                          Met Ser Thr Asn
19                                          1
20      cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag      102
21      Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
22      5                               10                               15                               20
23      gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg      150
24      Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
25      25                               30                               35
26      ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act      198
27      Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
28      40                               45                               50
29      tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca      246
30      Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
31      55                               60                               65
32      cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc      294
33      Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
34      70                               75                               80
35      ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc      342
36      Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
37      85                               90                               95                               100
38      agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg      390
39      Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser
40      105                               110                               115
41      cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat      438
42      Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
43      120                               125                               130
44      ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc      486

```

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/201,916

DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

```

45      Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
46              135                      140                      145
47      agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat      534
48      Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
49              150                      155                      160
50      gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc      582
51      Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
52      165                      170                      175                      180
53      ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac      630
54      Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
55              185                      190                      195
56      <210> SEQ ID NO 2
57      <211> LENGTH: 60
58      <212> TYPE: DNA
59      <213> ORGANISM: Hepatitis C Virus
60      <220> FEATURE:
61      <221> NAME/KEY: CDS
62      <222> LOCATION: (1)...(60)
63      <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
64      <400> SEQUENCE: 2
65      acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc      48
66      Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
67      1                      5                      10                      15
68      ggc gcc cct ctt
69      Gly Ala Pro Leu
70              20
71      <210> SEQ ID NO 3
72      <211> LENGTH: 18
73      <212> TYPE: DNA
74      <213> ORGANISM: Hepatitis C Virus
75      <220> FEATURE:
76      <221> NAME/KEY: CDS
77      <222> LOCATION: (1)...(18)
78      <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
79      <400> SEQUENCE: 3
80      ggt gtg aac tat gca aca
81      Gly Val Asn Tyr Ala Thr
82      1                      5
83      <210> SEQ ID NO 4
84      <211> LENGTH: 1900
85      <212> TYPE: DNA
86      <213> ORGANISM: Human
87      <400> SEQUENCE: 4
88      cgtcttcggg acgcgcccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag      60
89      gaagaaaaat ggcattccgtt gcagttgatc cacaaccgag tgttggtgact cgggtggtca      120
90      acctgccctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaagg      180
91      accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca      240
92      cctccgtggc catgaccagt gctctgccc tcatccagaa gctagagccg caaattgcag      300
93      ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga      360
94      atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg      420

```

PAGE: 3

RAW SEQUENCE LISTING PATENT APPLICATION US/09/201,916

DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

W--> 95 ctgtgacgac tactgtgact ggggccaaagg attctgtngc cagcacgacg acaggggtga 480
 96 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagtg 540
 97 gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgtagaaa 600
 98 atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac 660
 99 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg 720
 100 ttagactggg atccctgtct accaagcttc actcccgtgc ctaccagcag gctctcagca 780
 101 ggggttaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840
 102 acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgctc 900
 103 aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg 960
 104 atgagtccca ctgtgctgag cacattgagt cacgtactct tgcaattgcc cgcaacctga 1020
 105 ctgagcagct ccagaccacg tgccacaccc tctgtccaa catccaaggt gtaccacaga 1080
 106 acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc 1140
 107 gcaatgctgc ctccctttaa gaagtgtctg acagcctcct cacttctagc aaggggcagc 1200
 108 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttggtaac aacacgcccc 1260
 109 tcaactggct ggtaggtccc ttttatctc agctgactga gtctcagaat gctcaggacc 1320
 110 aagggtgcaga gatggacaag agcagccagg agaccagcg atctgagcat aaaactcatt 1380
 111 aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt 1440
 112 gaaattaact tgctaggcaa ccctaaattg ggaagcaagt agctagtata aaggccctca 1500
 113 attgtagttg tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
 114 ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
 115 aaaattcaaa tgcacttatg ttctcattct atggccattg tgttgccctct gttactgttt 1680
 116 gtattgaata aaaacatctt catgtgggct ggggtagaaa ctggtgtctg ctctgggtgtg 1740
 117 atctgaaaag gcgtcttcac tgctttatct catgatgctt gcttgtaaaa cttgatttta 1800
 118 gtttttctt tctcaaatag gaatactacc tttgaattca ataaaattca ctgcaggata 1860
 W--> 119 gaccagttta gtagcaaaaca nncaggtaca onnaagaaac 1900
 120 <210> SEQ ID NO 5
 121 <211> LENGTH: 437
 122 <212> TYPE: PRT
 123 <213> ORGANISM: Human
 124 <400> SEQUENCE: 5
 125 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
 126 1 5 10 15
 127 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
 128 20 25 30
 129 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
 130 35 40 45
 W--> 131 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
 132 50 55 60
 133 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
 134 65 70 75 80
 135 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
 136 85 90 95
 137 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
 138 100 105 110
 139 Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp
 140 115 120 125
 141 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
 142 130 135 140
 143 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
 144 145 150 155 160

See item 10 on Enn Summary Sheet

item 10

PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/09/201,916

DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

```

145   Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
146                               165                               170                               175
147   Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
148                               180                               185                               190
149   Leu Thr Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
150                               195                               200                               205
151   Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
152                               210                               215                               220
153   Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
154   225                               230                               235                               240
155   Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
156                               245                               250                               255
157   Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
158                               260                               265                               270
159   Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
160   275                               280                               285
161   Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
162   290                               295                               300
163   His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
164   305                               310                               315                               320
165   Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
166                               325                               330                               335
167   Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
168   340                               345                               350
169   Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
170   355                               360                               365
171   Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
172   370                               375                               380
173   Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
174   385                               390                               395                               400
175   Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
176   405                               410                               415
177   Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
178   420                               425                               430
179   Glu His Lys Thr His
180   435
181   <210> SEQ ID NO 6
182   <211> LENGTH: 31
183   <212> TYPE: PRT
184   <213> ORGANISM: Artificial Sequence
185   <220> FEATURE:
186   <223> OTHER INFORMATION: A branched peptide containing residues 5-27 of the
187   HCV core protein with degeneracy at positions 1
188   and 12 in which position 1 can be Ala or Pro and
189   position 12 can be Ile or Asn.
190   <400> SEQUENCE: 6
191   Ala Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Ile Arg Arg Pro Gln
192   1 5 10 15
193   Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
194   20 25 30

```

use Xaa and explain
in C2207-C2237 section

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/201,916DATE: 12/30/1999
TIME: 15:16:58

Input Set: I201916.RAW

195 <210> SEQ ID NO 7
196 <211> LENGTH: 11
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
201 protein deletion plasmids.
202 <400> SEQUENCE: 7
203 gctgagatct a 11
204 <210> SEQ ID NO 8
205 <211> LENGTH: 29
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
210 protein deletion plasmids.
211 <400> SEQUENCE: 8
212 gtaaccttcc tgggtgctct tgagatcta 29
213 <210> SEQ ID NO 9
214 <211> LENGTH: 17
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
219 protein deletion plasmids.
220 <400> SEQUENCE: 9
221 gtaacctttg agatcta 17
222 <210> SEQ ID NO 10
223 <211> LENGTH: 18
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
228 protein deletion plasmids.
229 <400> SEQUENCE: 10
230 ctggcgcatc gagatcta 18
231 <210> SEQ ID NO 11
232 <211> LENGTH: 28
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Oligonucleotides used to construct HCV core
237 protein deletion plasmids.
238 <400> SEQUENCE: 11
239 ctggcccatg gtgttaacta tgcaacag 28
240 <210> SEQ ID NO 12
241 <211> LENGTH: 31
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:

Input Set: I201916.RAW

Line	? Error/Warning	Original Text
95	W "N" or "Xaa" used: Feature required	ctgtgacgac tactgtgact ggggccaagg attctgtn
119	W "N" or "Xaa" used: Feature required	gaccagttna gnagcaaaca nncangtaca cnaagan
131	W "N" or "Xaa" used: Feature required	Met Xaa Glu Asn Gly Val Lys Thr Ile Thr S